



#3

SEQUENCE LISTING

<110> Hobbs, Helen H.  
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Tularik Inc.  
Board of Regents, The University of Texas System

<120> ABCG5 and ABCG8: Compositions and Methods of Use

<130> 018781-007320US

<140> US 09/989,981

<141> 2001-11-20

<150> US 60/252,235

<151> 2000-11-20

<150> US 60/253,645

<151> 2000-11-28

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1959

<212> DNA

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<221> CDS

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aca gag gct cgg cac agc tta ggt gtc ctg cat gtg tcc tac agc gtc 144  
Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val  
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Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys  
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tgg gac agg caa atc ctc aaa gat gtc tcc ttg tac atc gag agt ggc 240  
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cag att atg tgc atc tta ggc agc tca ggc tca ggg aag acc acg ctg 288  
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ctg gac gcc atc tcc ggg agg ctg cgg cgc act ggg acc ctg gaa ggg 336  
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gag gtg ttt gtg aat ggc tgc gag ctg cgc agg gac cag ttc caa gac 384  
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 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu  
 165 170 175

agc ctg agc cac gtg gcg gac caa atg att ggc agc tat aat ttt ggg 576  
 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly  
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gga att tcc agt ggc gag cgg cgc cga gtt tcc atc gca gcc caa ctc 624  
 Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu  
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ctt cag gac ccc aag gtc atg atg cta gat gag cca acc aca gga ctg 672  
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 210 215 220

gac tgc atg act gca aat caa att gtc ctt ctc ttg gct gag ctg gct 720  
 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala  
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cgc agg gac cga att gtg att gtc acc atc cac cag cct cgc tct gag 768  
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ttg aca tca gtg gac acc caa agc aga gag cgg gaa ata gaa acg tac 960  
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aag cga gta cag atg ctg gaa tgt gcc ttc aag gaa tct gac atc tat 1008  
 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr  
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cac aaa att ctg gag aac att gaa aga gca cga tac ctg aaa acc tta 1056  
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ccc atg gtt cct ttc aaa aca aaa gat cct cct ggg atg ttc ggc aag 1104  
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gtt gcc aga ttt gga tat ttc tct gct gct ctt ttg gcc cct cac tta 1536  
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att gga gaa ttt cta aca ctt gtg ctg ctt ggt ata gtc caa aac cct 1584  
 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro  
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aat att gtc aac agt ata gtg gct ctg ctc agc atc tct ggg ctg ctt 1632  
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att gga tct gga ttt atc aga aac ata caa gaa atg ccc att cct tta 1680  
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aaa atc ctg ggt tat ttt aca ttc caa aaa tac tgt tgt gag att ctc 1728  
 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu  
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gtg gtc aat gag ttt tac ggc ctg aac ttc act tgt ggt gga tcc aac 1776  
Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn  
580 585 590

acc tct atg cta aat cac ccg atg tgc gcc atc acc caa ggg gtc cag 1824  
Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln  
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ttc atc gag aaa acc tgc cca ggt gct aca tcc aga ttc acg gca aac 1872  
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Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val  
35 40 45  
Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys  
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Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu  
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Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly  
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Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp  
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Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr  
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Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser  
145 150 155 160  
Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu  
165 170 175  
Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly  
180 185 190  
Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu  
195 200 205  
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210 215 220  
Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala  
225 230 235 240

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 245 250 255  
 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu  
 260 265 270  
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 275 280 285  
 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp  
 290 295 300  
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 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr  
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 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu  
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 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys  
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 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala  
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 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met  
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 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu  
 485 490 495  
 Val Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu  
 500 505 510  
 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro  
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 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu  
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 545 550 555 560  
 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu  
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 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn  
 580 585 590  
 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln  
 595 600 605  
 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn  
 610 615 620  
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gac aac agt ctg tac ttc acc tac agt ggt cag tcc aac act ctg gag 144  
 Asp Asn Ser Leu Tyr Phe Thr Tyr Ser Gly Gln Ser Asn Thr Leu Glu  
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gtc aga gat ctc acc tac cag gtg gac atc gcc tct cag gtg cct tgg 192  
 Val Arg Asp Leu Thr Tyr Gln Val Asp Ile Ala Ser Gln Val Pro Trp  
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ttt gag cag ctg gct cag ttc aag ata ccc tgg agg tct cat agc agc 240  
 Phe Glu Gln Leu Ala Gln Phe Lys Ile Pro Trp Arg Ser His Ser Ser  
 65 70 75 80

caa gac tcc tgt gag ctg ggc atc cga aat cta agc ttc aaa gtg agg 288  
 Gln Asp Ser Cys Glu Leu Gly Ile Arg Asn Leu Ser Phe Lys Val Arg  
 85 90 95

agt gga cag atg ctg gcc atc ata ggg agc tca ggc tgc ggg aga gcc 336  
 Ser Gly Gln Met Leu Ala Ile Ile Gly Ser Ser Gly Cys Gly Arg Ala  
 100 105 110

tca cta ctc gac gtg atc aca ggc aga ggc cac ggt ggc aag atg aaa 384  
 Ser Leu Leu Asp Val Ile Thr Gly Arg Gly His Gly Gly Lys Met Lys  
 115 120 125

tca gga caa att tgg ata aat ggg caa ccc agt acg cct cag ctg gtg 432  
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agg aag tgc gtt gcg cat gtg cgg cag cat gac caa ctg ctg ccc aac 480  
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 145 150 155 160

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 165 170 175

agg acc ttc tcc cag gcc cag cgt gac aaa cgg gtg gaa gac gta atc 576  
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 180 185 190

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tat gta cgt ggg gtg tcc ggg ggt gag cgc cga cga gtg agc att ggg 672  
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 225 230 235 240

tct ggc ctc gac agc ttc aca gcc cac aat ctg gtg aca acc ttg tcc 768  
 Ser Gly Leu Asp Ser Phe Thr Ala His Asn Leu Val Thr Thr Leu Ser  
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cgc ctg gcc aag ggc aac agg ctg gtg ctc atc tcc ctc cac cag cct 816  
 Arg Leu Ala Lys Gly Asn Arg Leu Val Leu Ile Ser Leu His Gln Pro  
 260 265 270

cgc tct gac atc ttc agg cta ttt gac ctg gtc ctt ctg atg aca tct 864  
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ggc acc cct atc tac ctg ggg gcg gcg cag caa atg gtg cag tac ttc 912  
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aca tcc att ggc cac cct tgt cct cgc tat agc aac cct gcg gac ttc 960  
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gcc acc gtg gag aag gca cag tct ctt gca gcc ctg ttc cta gaa aaa 1056  
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ctg atc cgt cgt cag att tcc aat gac ttc cgg gac ctg ccc acg ctg 1248  
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625 630 635 640  
  
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Ala Ile Tyr Leu Ile Val Ile Gly Ile Ser Tyr Gly Phe Leu Phe Leu  
645 650 655  
  
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660 665 670  
  
tga 2019

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Val Arg Asp Leu Thr Tyr Gln Val Asp Ile Ala Ser Gln Val Pro Trp  
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Phe Glu Gln Leu Ala Gln Phe Lys Ile Pro Trp Arg Ser His Ser Ser  
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85 90 95  
Ser Gly Gln Met Leu Ala Ile Ile Gly Ser Ser Gly Cys Gly Arg Ala  
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Ser Leu Leu Asp Val Ile Thr Gly Arg Gly His Gly Gly Lys Met Lys  
115 120 125  
Ser Gly Gln Ile Trp Ile Asn Gly Gln Pro Ser Thr Pro Gln Leu Val  
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180 185 190  
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260 265 270  
Arg Ser Asp Ile Phe Arg Leu Phe Asp Leu Val Leu Leu Met Thr Ser  
275 280 285  
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325 330 335  
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 545 550 555 560  
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 565 570 575  
 Ile Asn Leu Asp Asn Leu Trp Ile Val Pro Ala Trp Ile Ser Lys Leu  
 580 585 590  
 Ser Phe Leu Arg Trp Cys Phe Ser Gly Leu Met Gln Ile Gln Phe Asn  
 595 600 605  
 Gly His Leu Tyr Thr Thr Gln Ile Gly Asn Phe Thr Phe Ser Ile Leu  
 610 615 620  
 Gly Asp Thr Met Ile Ser Ala Met Asp Leu Asn Ser His Pro Leu Tyr  
 625 630 635 640  
 Ala Ile Tyr Leu Ile Val Ile Gly Ile Ser Tyr Gly Phe Leu Phe Leu  
 645 650 655  
 Tyr Tyr Leu Ser Leu Lys Leu Ile Lys Gln Lys Ser Ile Gln Asp Trp  
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 <213> Homo sapiens

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 <222> (107)..(2062)  
 <223> human ABCG5 (hABCG5)

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 Met Gly Asp  
 1  
 ctc tca tct ttg acc ccc gga ggg tcc atg ggt ctc caa gta aac aga 163  
 Leu Ser Ser Leu Thr Pro Gly Gly Ser Met Gly Leu Gln Val Asn Arg  
 5 10 15  
 ggc tcc cag agc tcc ctg gag ggg gct cct gcc acc gcc ccg gag cct 211  
 Gly Ser Gln Ser Ser Leu Glu Gly Ala Pro Ala Thr Ala Pro Glu Pro  
 20 25 30 35  
 cac agc ctg ggc atc ctc cat gcc tcc tac agc gtc agc cac cgc gtg 259  
 His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser His Arg Val  
 40 45 50

agg ccc tgg tgg gac atc aca tct tgc cgg cag cag tgg acc agg cag 307  
 Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp Thr Arg Gln  
 55 60 65

atc ctc aaa gat gtc tcc ttg tac gtg gag agc ggg cag atc atg tgc 355  
 Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln Ile Met Cys  
 70 75 80

atc cta gga agc tca ggc tcc ggg aaa acc acg ctg ctg gac gcc atg 403  
 Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu Asp Ala Met  
 85 90 95

tcc ggg agg ctg ggg cgc gcg ggg acc ttc ctg ggg gag gtg tat gtg 451  
 Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu Val Tyr Val  
 100 105 110 115

aac ggc cgg gcg ctg cgc cgg gag cag ttc cag gac tgc ttc tcc tac 499  
 Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys Phe Ser Tyr  
 120 125 130

gtc ctg cag agc gac acc ctg ctg agc agc ctc acc gtg cgc gag acg 547  
 Val Leu Gln Ser Asp Thr Leu Leu Ser Ser Leu Thr Val Arg Glu Thr  
 135 140 145

ctg cac tac acc gcg ctg ctg gcc atc cgc cgc ggc aat ccc ggc tcc 595  
 Leu His Tyr Thr Ala Leu Leu Ala Ile Arg Arg Gly Asn Pro Gly Ser  
 150 155 160

ttc cag aag aag gtg gag gcc gtc atg gca gag ctg agt ctg agc cat 643  
 Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser Leu Ser His  
 165 170 175

gtg gca gac cga ctg att ggc aac tac agc ttg ggg ggc att tcc acg 691  
 Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly Ile Ser Thr  
 180 185 190 195

ggt gag cgg cgc cgg gtc tcc atc gca gcc cag ctg ctc cag gat cct 739  
 Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu Leu Gln Asp Pro  
 200 205 210

aag gtc atg ctg ttt gat gag cca acc aca ggc ctg gac tgc atg act 787  
 Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp Cys Met Thr  
 215 220 225

gct aat cag att gtc gtc ctc ctg gtg gaa ctg gct cgc agg aac cga 835  
 Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg Arg Asn Arg  
 230 235 240

att gtg gtt ctc acc att cac cag ccc cgt tct gag ctt ttt cag ctc 883  
 Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu Phe Gln Leu  
 245 250 255

ttt gac aaa att gcc atc ctg agc ttc gga gag ctg att ttc tgt ggc 931  
 Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile Phe Cys Gly  
 260 265 270 275

acg cca gcg gaa atg ctt gat ttc ttc aat gac tgc ggt tac cct tgt 979  
 Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly Tyr Pro Cys  
 280 285 290

cct gaa cat tca aac cct ttt gac ttc tat atg gac ctg acg tca gtg 1027  
 Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu Thr Ser Val  
 295 300 305

gat acc caa agc aag gaa cgg gaa ata gaa acc tcc aag aga gtc cag 1075  
 Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys Arg Val Gln  
 310 315 320

atg ata gaa tct gcc tac aag aaa tca gca att tgt cat aaa act ttg 1123  
 Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His Lys Thr Leu  
 325 330 335

aag aat att gaa aga atg aaa cac ctg aaa acg tta cca atg gtt cct 1171  
 Lys Asn Ile Glu Arg Met Lys His Ile Lys Thr Leu Pro Met Val Pro  
 340 345 350 355

ttc aaa acc aaa gat tct cct gga gtt ttc tct aaa ctg ggt gtt ctc 1219  
 Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu Gly Val Leu  
 360 365 370

ctg agg aga gtg aca aga aac ttg gtg aga aat aag ctg gca gtg att 1267  
 Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu Ala Val Ile  
 375 380 385

acg cgt ctc ctt cag aat ctg atc atg ggt ttg ttc ctc ctt ttc ttc 1315  
 Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu Leu Phe Phe  
 390 395 400

gtt ctg cgg gtc cga agc aat gtg cta aag ggt gct atc cag gac cgc 1363  
 Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile Gln Asp Arg  
 405 410 415

gta ggt ctc ctt tac cag ttt gtg ggc gcc acc ccg tac aca ggc atg 1411  
 Val Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr Thr Gly Met  
 420 425 430 435

ctg aac gct gtg aat ctg ttt ccc gtg ctg cga gct gtc agc gac cag 1459  
 Leu Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val Ser Asp Gln  
 440 445 450

gag agt cag gac ggc ctc tac cag aag tgg cag atg atg ctg gcc tat 1507  
 Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met Leu Ala Tyr  
 455 460 465

gca ctg cac gtc ctc ccc ttc agc gtt gtt gcc acc atg att ttc agc 1555  
 Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met Ile Phe Ser  
 470 475 480

agt gtg tgc tac tgg acg ctg ggc tta cat cct gag gtt gcc cga ttt 1603  
 Ser Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val Ala Arg Phe  
 485 490 495

gga tat ttt tct gct gct ctc ttg gcc ccc cac tta att ggt gaa ttt 1651  
 Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile Gly Glu Phe  
 500 505 510 515

cta act ctt gtg cta ctt ggt atc gtc caa aat cca aat ata gtc aac 1699  
 Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn Ile Val Asn  
 520 525 530

agt gta gtg gct ctg ctg tcc att gcg ggg gtg ctt gtt gga tct gga 1747  
Ser Val Val Ala Leu Leu Ser Ile Ala Gly Val Leu Val Gly Ser Gly  
535 540 545

ttc ctc aga aac ata caa gaa atg ccc att cct ttt aaa atc atc agt 1795  
Phe Leu Arg Asn Ile Gln Glu Met Pro Ile Pro Phe Lys Ile Ile Ser  
550 555 560

tat ttt aca ttc caa aaa tat tgc agt gag att ctt gta gtc aat gag 1843  
Tyr Phe Thr Phe Gln Lys Tyr Cys Ser Glu Ile Leu Val Val Asn Glu  
565 570 575

ttc tac gga ctg aat ttc act tgt ggc agc tca aat gtt tct gtg aca 1891  
Phe Tyr Gly Leu Asn Phe Thr Cys Gly Ser Ser Asn Val Ser Val Thr  
580 585 590 595

act aat cca atg tgt gcc ttc act caa gga att caa ttc att gag aaa 1939  
Thr Asn Pro Met Cys Ala Phe Thr Gln Gly Ile Gln Phe Ile Glu Lys  
600 605 610

acc tgc cca ggt gca aca tct aga ttc aca atg aac ttt ctg att ttg 1987  
Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Met Asn Phe Leu Ile Leu  
615 620 625

tat tca ttt att cca gct ctt gtc atc cta gga ata gtt gtt ttc aaa 2035  
Tyr Ser Phe Ile Pro Ala Leu Val Ile Leu Gly Ile Val Val Phe Lys  
630 635 640

ata agg gat cat ctc att agc agg tag tgaaagccat ggctgggaaa 2082  
Ile Arg Asp His Leu Ile Ser Arg  
645 650

atggaagtga agctgccgac tgtgcatgac tgcctctgaac gtctgaaatg agagtgccat 2142

gtattttcttt cttgacagga catctcaagt cttttaacca ttaagactcc atttgtgcct 2202

cttggatcca agcaggcctt gaatgcaatg gaagtgggtt atagtccttt gctcttataa 2262

cttgcaggga catgtgggta tttggaaatt gtgactgagc ggaccaaga atgtaaataa 2322

tattcataaa cctatggg 2340

<210> 6

<211> 651

<212> PRT

<213> Homo sapiens

<220>

<223> human ABCG5 (hABCG5)

<400> 6

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20 25 30  
Pro Glu Pro His Ser Leu Gly Ile Leu His Ala Ser Tyr Ser Val Ser  
35 40 45  
His Arg Val Arg Pro Trp Trp Asp Ile Thr Ser Cys Arg Gln Gln Trp  
50 55 60

Thr Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Val Glu Ser Gly Gln  
 65 70 75 80  
 Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu Leu  
 85 90 95  
 Asp Ala Met Ser Gly Arg Leu Gly Arg Ala Gly Thr Phe Leu Gly Glu  
 100 105 110  
 Val Tyr Val Asn Gly Arg Ala Leu Arg Arg Glu Gln Phe Gln Asp Cys  
 115 120 125  
 Phe Ser Tyr Val Leu Gln Ser Asp Thr Leu Leu Ser Ser Leu Thr Val  
 130 135 140  
 Arg Glu Thr Leu His Tyr Thr Ala Leu Leu Ala Ile Arg Arg Gly Asn  
 145 150 155 160  
 Pro Gly Ser Phe Gln Lys Lys Val Glu Ala Val Met Ala Glu Leu Ser  
 165 170 175  
 Leu Ser His Val Ala Asp Arg Leu Ile Gly Asn Tyr Ser Leu Gly Gly  
 180 185 190  
 Ile Ser Thr Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu Leu  
 195 200 205  
 Gln Asp Pro Lys Val Met Leu Phe Asp Glu Pro Thr Thr Gly Leu Asp  
 210 215 220  
 Cys Met Thr Ala Asn Gln Ile Val Val Leu Leu Val Glu Leu Ala Arg  
 225 230 235 240  
 Arg Asn Arg Ile Val Val Leu Thr Ile His Gln Pro Arg Ser Glu Leu  
 245 250 255  
 Phe Gln Leu Phe Asp Lys Ile Ala Ile Leu Ser Phe Gly Glu Leu Ile  
 260 265 270  
 Phe Cys Gly Thr Pro Ala Glu Met Leu Asp Phe Phe Asn Asp Cys Gly  
 275 280 285  
 Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp Leu  
 290 295 300  
 Thr Ser Val Asp Thr Gln Ser Lys Glu Arg Glu Ile Glu Thr Ser Lys  
 305 310 315 320  
 Arg Val Gln Met Ile Glu Ser Ala Tyr Lys Lys Ser Ala Ile Cys His  
 325 330 335  
 Lys Thr Leu Lys Asn Ile Glu Arg Met Lys His Leu Lys Thr Leu Pro  
 340 345 350  
 Met Val Pro Phe Lys Thr Lys Asp Ser Pro Gly Val Phe Ser Lys Leu  
 355 360 365  
 Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Val Arg Asn Lys Leu  
 370 375 380  
 Ala Val Ile Thr Arg Leu Leu Gln Asn Leu Ile Met Gly Leu Phe Leu  
 385 390 395 400  
 Leu Phe Phe Val Leu Arg Val Arg Ser Asn Val Leu Lys Gly Ala Ile  
 405 410 415  
 Gln Asp Arg Val Gly Leu Leu Tyr Gln Phe Val Gly Ala Thr Pro Tyr  
 420 425 430  
 Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Val Leu Arg Ala Val  
 435 440 445  
 Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr Gln Lys Trp Gln Met Met  
 450 455 460  
 Leu Ala Tyr Ala Leu His Val Leu Pro Phe Ser Val Val Ala Thr Met  
 465 470 475 480  
 Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu His Pro Glu Val  
 485 490 495  
 Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu Ile  
 500 505 510  
 Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro Asn  
 515 520 525  
 Ile Val Asn Ser Val Val Ala Leu Leu Ser Ile Ala Gly Val Leu Val  
 530 535 540

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Gly | Phe | Leu | Arg | Asn | Ile | Gln | Glu | Met | Pro | Ile | Pro | Phe | Lys |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Ile | Ile | Ser | Tyr | Phe | Thr | Phe | Gln | Lys | Tyr | Cys | Ser | Glu | Ile | Leu | Val |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     |     | 575 |
| Val | Asn | Glu | Phe | Tyr | Gly | Leu | Asn | Phe | Thr | Cys | Gly | Ser | Ser | Asn | Val |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ser | Val | Thr | Thr | Asn | Pro | Met | Cys | Ala | Phe | Thr | Gln | Gly | Ile | Gln | Phe |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Ile | Glu | Lys | Thr | Cys | Pro | Gly | Ala | Thr | Ser | Arg | Phe | Thr | Met | Asn | Phe |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Leu | Ile | Leu | Tyr | Ser | Phe | Ile | Pro | Ala | Leu | Val | Ile | Leu | Gly | Ile | Val |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Val | Phe | Lys | Ile | Arg | Asp | His | Leu | Ile | Ser | Arg |     |     |     |     |     |
|     |     |     |     | 645 |     |     |     |     |     | 650 |     |     |     |     |     |

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 <213> Homo sapiens

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 <222> (100)..(2121)  
 <223> human ABCG8 (hABCG8)

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 aagagagctg cagcccaggg tcacagacct gtgggcccc atg gcc ggg aag gcc 114  
 Met Ala Gly Lys Ala  
 1 5  
 gca gag gag aga ggg ctg ccg aaa ggg gcc act ccc cag gat acc tcg 162  
 Ala Glu Glu Arg Gly Leu Pro Lys Gly Ala Thr Pro Gln Asp Thr Ser  
 10 15 20  
 ggc ctc cag gat aga ttg ttc tcc tct gaa agt gac aac agc ctg tac 210  
 Gly Leu Gln Asp Arg Leu Phe Ser Ser Glu Ser Asp Asn Ser Leu Tyr  
 25 30 35  
 ttc acc tac agt ggc cag ccc aac acc ctg gag gtc aga gac ctc aac 258  
 Phe Thr Tyr Ser Gly Gln Pro Asn Thr Leu Glu Val Arg Asp Leu Asn  
 40 45 50  
 tac cag gtg gac ctg gcc tct cag gtc cct tgg ttt gag cag ctg gct 306  
 Tyr Gln Val Asp Leu Ala Ser Gln Val Pro Trp Phe Glu Gln Leu Ala  
 55 60 65  
 cag ttc aag atg ccc tgg aca tct ccc agc tgc cag aat tct tgt gag 354  
 Gln Phe Lys Met Pro Trp Thr Ser Pro Ser Cys Gln Asn Ser Cys Glu  
 70 75 80 85  
 ctg ggc atc cag aac cta agc ttc aaa gtg aga agt ggg cag atg ctg 402  
 Leu Gly Ile Gln Asn Leu Ser Phe Lys Val Arg Ser Gly Gln Met Leu  
 90 95 100  
 gcc atc ata ggg agc tca ggt tgt ggg aga gcc tcc ttg cta gat gtg 450  
 Ala Ile Ile Gly Ser Ser Gly Cys Gly Arg Ala Ser Leu Leu Asp Val  
 105 110 115

atc act ggc cga ggt cac ggc ggc aag atc aag tca ggc cag atc tgg 498  
 Ile Thr Gly Arg Gly His Gly Gly Lys Ile Lys Ser Gly Gln Ile Trp  
 120 125 130

atc aat ggg cag ccc agc tgg cct cag ctg gtg agg aag tgt gtg gcc 546  
 Ile Asn Gly Gln Pro Ser Ser Pro Gln Leu Val Arg Lys Cys Val Ala  
 135 140 145

cac gtg cgc cag cac aac cag ctg ctc ccc aac ttg act gtg cga gag 594  
 His Val Arg Gln His Asn Gln Leu Leu Pro Asn Leu Thr Val Arg Glu  
 150 155 160 165

acc ttg gcc ttc att gcc cag atg cgg ctg ccc aga acc ttc tcc cag 642  
 Thr Leu Ala Phe Ile Ala Gln Met Arg Leu Pro Arg Thr Phe Ser Gln  
 170 175 180

gcc cag cgt gac aaa agg gtg gag gac gtg atc gcg gag ctg cgg ctt 690  
 Ala Gln Arg Asp Lys Arg Val Glu Asp Val Ile Ala Glu Leu Arg Leu  
 185 190 195

agg cag tgc gct gac acc cgc gtg ggc aac atg tac gtg cgg ggg ttg 738  
 Arg Gln Cys Ala Asp Thr Arg Val Gly Asn Met Tyr Val Arg Gly Leu  
 200 205 210

tgc ggg ggt gag cgc agg aga gtc agc att ggg gtg cag ctc ctg tgg 786  
 Ser Gly Gly Glu Arg Arg Arg Val Ser Ile Gly Val Gln Leu Leu Trp  
 215 220 225

aac cca gga atc ctt att ctc gac gaa ccc acc tct ggg ctc gac agc 834  
 Asn Pro Gly Ile Leu Ile Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser  
 230 235 240 245

ttc aca gcc cac aac ctg gtg aag acc ttg tcc agg ctg gcc aaa ggc 882  
 Phe Thr Ala His Asn Leu Val Lys Thr Leu Ser Arg Leu Ala Lys Gly  
 250 255 260

aac cgg ctg gtg ctc atc tcc ctc cac cag cct cgc tct gac atc ttc 930  
 Asn Arg Leu Val Leu Ile Ser Leu His Gln Pro Arg Ser Asp Ile Phe  
 265 270 275

agg ctg ttt gat ctg gtc ctc ctg atg acg tct ggc acc ccc atc tac 978  
 Arg Leu Phe Asp Leu Val Leu Leu Met Thr Ser Gly Thr Pro Ile Tyr  
 280 285 290

tta ggg gcg gcc cag cac atg gtc cag tat ttc aca gcc atc ggc tac 1026  
 Leu Gly Ala Ala Gln His Met Val Gln Tyr Phe Thr Ala Ile Gly Tyr  
 295 300 305

ccc tgt cct cgc tac agc aat cct gct gac ttc tat gtg gac ctg acc 1074  
 Pro Cys Pro Arg Tyr Ser Asn Pro Ala Asp Phe Tyr Val Asp Leu Thr  
 310 315 320 325

agc att gac agg cgc agc aga gag cag gaa ttg gcc acc agg gag aag 1122  
 Ser Ile Asp Arg Arg Ser Arg Glu Gln Glu Leu Ala Thr Arg Glu Lys  
 330 335 340

gct cag tca ctc gca gcc ctg ttt cta gaa aaa gtg cgt gac tta gat 1170  
 Ala Gln Ser Leu Ala Ala Leu Phe Leu Glu Lys Val Arg Asp Leu Asp  
 345 350 355



gac ttt cta tgg aaa gca gag acg aag gat ctt gac gag gac acc tgt 1218  
 Asp Phe Leu Trp Lys Ala Glu Thr Lys Asp Leu Asp Glu Asp Thr Cys  
 360 365 370

gtg gaa agc agc gtg acc cca cta gac acc aac tgc ctc ccg agt cct 1266  
 Val Glu Ser Ser Val Thr Pro Leu Asp Thr Asn Cys Leu Pro Ser Pro  
 375 380 385

acg aag atg cct ggg gcg gtg cag cag ttt acg acg ctg atc cgt cgt 1314  
 Thr Lys Met Pro Gly Ala Val Gln Gln Phe Thr Thr Leu Ile Arg Arg  
 390 395 400 405

cag att tcc aac gac ttc cga gac ctg ccc acc ctc ctc atc cat ggg 1362  
 Gln Ile Ser Asn Asp Phe Arg Asp Leu Pro Thr Leu Leu Ile His Gly  
 410 415 420

gcg gag gcc tgt ctg atg tca atg acc atc ggc ttc ctc tat ttt ggc 1410  
 Ala Glu Ala Cys Leu Met Ser Met Thr Ile Gly Phe Leu Tyr Phe Gly  
 425 430 435

cat ggg agc atc cag ctc tcc ttc atg gat aca gcc gcc ctc ttg ttc 1458  
 His Gly Ser Ile Gln Leu Ser Phe Met Asp Thr Ala Ala Leu Leu Phe  
 440 445 450

atg atc ggt gct ctc atc cct ttc aac gtc att ctg gat gtc atc tcc 1506  
 Met Ile Gly Ala Leu Ile Pro Phe Asn Val Ile Leu Asp Val Ile Ser  
 455 460 465

aaa tgt tac tca gag agg gca atg ctt tac tat gaa ctg gaa gac ggg 1554  
 Lys Cys Tyr Ser Glu Arg Ala Met Leu Tyr Tyr Glu Leu Glu Asp Gly  
 470 475 480 485

ctg tac acc act ggt cca tat ttc ttt gcc aag atc ctc ggg gag ctt 1602  
 Leu Tyr Thr Thr Gly Pro Tyr Phe Phe Ala Lys Ile Leu Gly Glu Leu  
 490 495 500

ccg gag cac tgt gcc tac atc atc atc tac ggg atg ccc acc tac tgg 1650  
 Pro Glu His Cys Ala Tyr Ile Ile Ile Tyr Gly Met Pro Thr Tyr Trp  
 505 510 515

ctg gcc aac ctg agg cca ggc ctc cag ccc ttc ctg ctg cac ttc ctg 1698  
 Leu Ala Asn Leu Arg Pro Gly Leu Gln Pro Phe Leu Leu His Phe Leu  
 520 525 530

ctg gtg tgg ctg gtg gtc ttc tgt tgc agg att atg gcc ctg gcc gcc 1746  
 Leu Val Trp Leu Val Val Phe Cys Cys Arg Ile Met Ala Leu Ala Ala  
 535 540 545

gcg gcc ctg ctc ccc acc ttc cac atg gcc tcc ttc ttc agc aat gcc 1794  
 Ala Ala Leu Leu Pro Thr Phe His Met Ala Ser Phe Phe Ser Asn Ala  
 550 555 560 565

ctc tac aac tcc ttc tac ctc gcc ggg ggc ttc atg ata aac ttg agc 1842  
 Leu Tyr Asn Ser Phe Tyr Leu Ala Gly Gly Phe Met Ile Asn Leu Ser  
 570 575 580

agc ctg tgg aca gtg ccc gcg tgg att toc aaa gtg tcc ttc ctg cgg 1890  
 Ser Leu Trp Thr Val Pro Ala Trp Ile Ser Lys Val Ser Phe Leu Arg  
 585 590 595

tgg tgt ttt gaa ggg ctg atg aag att cag ttc agc aga aga act tat 1938  
Trp Cys Phe Glu Gly Leu Met Lys Ile Gln Phe Ser Arg Arg Thr Tyr  
600 605 610

aaa atg cct ctc ggg aac ctc acc atc gcg gtc tca gga gat aaa atc 1986  
Lys Met Pro Leu Gly Asn Leu Thr Ile Ala Val Ser Gly Asp Lys Ile  
615 620 625

ctc agt gcc atg gag ctg gac tcg tac cct ctc tac gcc atc tac ctc 2034  
Leu Ser Ala Met Glu Leu Asp Ser Tyr Pro Leu Tyr Ala Ile Tyr Leu  
630 635 640 645

atc gtc att ggc ctc agc ggt ggc ttc atg gtc ctg tac tac gtg tcc 2082  
Ile Val Ile Gly Leu Ser Gly Gly Phe Met Val Leu Tyr Tyr Val Ser  
650 655 660

tta agg ttc atc aaa cag aaa cca agt caa gac tgg tga ttcacgccag 2131  
Leu Arg Phe Ile Lys Gln Lys Pro Ser Gln Asp Trp  
665 670

acgtctgccc gctggtgggg gacctgagca gacccttcaa ctgcactccc tctcaggag 2191

ccccttctg gggacagtga ggacaatgac cctacagatg ctcagctaca tccggcccag 2251

ggtgctgcag tggcacagac cagccacagg atggcagtag aataaagaca gtcgaaaggg 2311

atttctgctc actggcagga gactgcgatg actgggagaa aacctgcact cgggtggcacc 2371

tacaacgttg ctaatttatt tcttttgat atgcatttat ataggcaact cgatatagga 2431

tgggagcaaa ctaggaatga attgggtagc tagactgtgc aggaattggt ggaacctgga 2491

gggaacaata acagtagcta gcagatttggt cttcatcttc cagggggcccc acactccgtg 2551

gtgagccacc atcaatacag aaagtgacct aagatgtacc agcaagatgc catcccttct 2611

ttttgtgtgg ggtcatgggc tccaaaagcc aacgtgaaca attaaaaatg tattgagc 2669

<210> 8

<211> 673

<212> PRT

<213> Homo sapiens

<220>

<223> human ABCG8 (hABCG8)

<400> 8

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Pro Gln Asp Thr Ser Gly Leu Gln Asp Arg Leu Phe Ser Ser Glu Ser  
20 25 30  
Asp Asn Ser Leu Tyr Phe Thr Tyr Ser Gly Gln Pro Asn Thr Leu Glu  
35 40 45  
Val Arg Asp Leu Asn Tyr Gln Val Asp Leu Ala Ser Gln Val Pro Trp  
50 55 60  
Phe Glu Gln Leu Ala Gln Phe Lys Met Pro Trp Thr Ser Pro Ser Cys  
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 Phe Leu Tyr Phe Gly His Gly Ser Ile Gln Leu Ser Phe Met Asp Thr  
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 (forward strand)

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25  
25/11

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